

1/27

FIG. 1

NUCLEIC ACID AND PREDICTED PROTEIN SEQUENCE OF DZ2

NcoI

```

1  GGCACGAGCAGAATCGAAGATGGCAACAATAATCCATGGGAGATATCGAGAAATAAGAA 60
   M A T K S M G D I E K I K K

61  GAACTAAACGTGTGATCGTCGATGATCCACTAACCTTATAATTATGAGAAGAT 120
   K L N V L I V D D D P L N L I I H E K I

121 CATCAAAGCGATTGGGGGTATTTACACAGACAGCGGAATAACGGTGAGGAGGCAGTAATCAT 180
   I K A I G G I S Q T A N N G E E A V I I
       ↓
       DZ2FL→

181 CCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCGAGAG 240
   H R D G G S S F D L I L M D K E M P E R

241 GGATGGTGTTCGACAACCTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGG 300
   D G V S T T K K L R E M E V K S M I V G

301 GGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTTCATGGAAGCTGGACTTAA 360
   V T S L A D N E E E R R A F M E A G L N
  
```

2/27

```

361 CCATTGCTGGCAAAACCGTTAACCAAGACAAGATCATCCCTCTCATTAACCAACTCAT 420
    H C L A K P L T K D K I I P L I N Q L M
    ← DZ2RL
421 GGATGCTTGATGGATATATATTTATATGGAACACACATAATAACGTCTAAGTGTG 480
    D A *
481 TATGATGCATAGATAGATACTTGCATGTTGTGTTTAGAATTTAGGGTTCTTTATCGTCCGT 540
    HindIII
541 GATATATAATCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTAAATAAGGGTTTCCT 600
601 CTACC
    
```

The primer sites for DZ2FL and DZ2RL are underlined, as are the recognition sequences for *Nco*I and *Hind*III restriction enzymes. Shown in bold are the conserved amino acid residues required for phosphorylation. The extent of the original PCR product isolated by differential display is shown by ↓.

FIG. 1 CONT'D

3/27

Alignment of the predicted protein sequence of DZ2 with those of
bacterial response regulator proteins.

	1				50
DZ2	MATKSMGDIE	KIKKKLNVLI	VDDDPLNLII	HEKIIKAIG.	GISQTANNGE
OMPRMQENYKILV	VDDDMRLRAL	LERYLTEQGF	.QVRSVANAE
PHOBMARRILV	VEDEAPIREM	VCFVLEQNGF	.QPVEAEDYD
NTRCMQRGIVWV	VDDSSIRWV	LERALAGAGL	.TCTTFENG
SPOOFMMNEKILI	VDDQYGIRIL	LNEVFNKEGY	.QTFQAANGL
CHEY	MADKELKFLV	VDDFSTMRRI	VRNLLKELGF	NNVEEAEDGV
ETRLKVLV	MDENGVSVMV	TKGLLVHLGC	EVTTVSSNEE
	51				100
DZ2	EAVIIHRDGG	SSFDLILMDK	EMPERDGVST	TKKLREMEVK	SM..IVGVTS
OMPR	QMDRLLTR..	ESFHLMVLDL	MLPGEDGLSI	CRRLRSQS..	NPMPIIMVTA
PHOB	SAVNQLNE..	PWPDILLDW	MLPGGSGIQF	IKHLKRESMT	RDIPVVMLTA
NTRC	EVLAALAS..	KTPDVLLSDI	RMPGMDGLAL	LKQIKQ..RH	PMLPVIIMTA
SPOOF	QALDIVTK..	ERPDLVLLDM	KIPGMDGIEI	LKRMKV..ID	ENIRVIIMTA
CHEY	DALNKLQA..	GGYGFVISDW	NMPNMDGLEL	LKTIRADGAM	SALPVLIMVTA
ETRCLRVVS	HEHKVVFMDV	CMPGVENYQI	ALRI.....	.HXPLLVALS
	101				150
DZ2	LADNEEERRA	FMEAGLNHCL	AKPLTKDKII	PLINQLMDA.
OMPR	KGEEVDRIVG	.LEIGADDYI	PKPFNPPELL	ARIRAVLRRQ	ANELPGAPS.
PHOB	RGEEEDRVRG	.LETGADDYI	TKPFSPKELV	ARIKAVMRRI	SPM.....
NTRC	HSDLDAVSA	.YQQGAFDYL	PKPFDIDEAV	ALVERAISHY	QEQQOPRNI
SPOOF	YGELDMIQES	.KELGALTHF	AKPFDIDEIR	DAVKKYLPLK	SN.....
CHEY	EAKKENIIAA	.AQAGASGYV	VKPFTPATLE	EKLNKIFEKL	GM.....
ETR	GNTDKSTKEK	CMSFGLDGLV	LKPVS LDNIR	DVLSDLL...
	151				
DZ2				
OMPR	OmpR = <i>E. coli</i>	(Involved in osmoregulation)		
PHOB	PhoB = <i>E. coli</i>	(Involved in phosphate utilisation)		
NTRC	VNGP	NtrC = <i>S. typhimurium</i>	(Involved in nitrogen utilisation)		
SPOOF	SpoOF = <i>B. subtilis</i>	(Involved in sporulation)		
CHEY	CheY = <i>E. coli</i>	(Involved in chemotaxis)		
ETR	ETR = <i>A. thaliana ETR1</i> gene	encoding an ethylene receptor (partial amino acid sequence)		

The predicted protein sequence of DZ2 is shown in bold as are the conserved amino acid residues required for phosphorylation of the protein

FIG. 2

4/27

Expression analysis of DZ2 in various plant organs using Northern

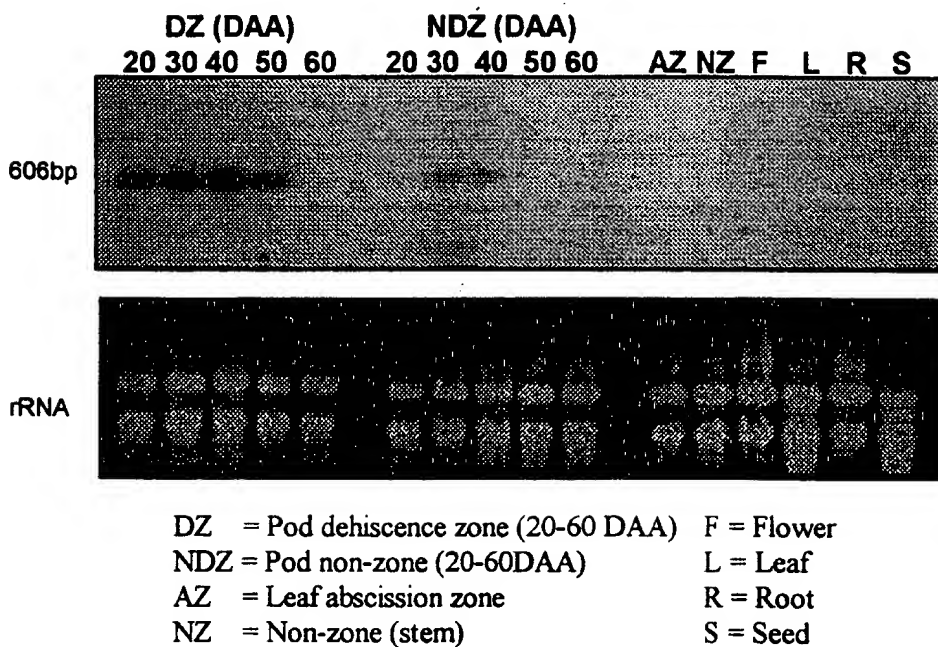
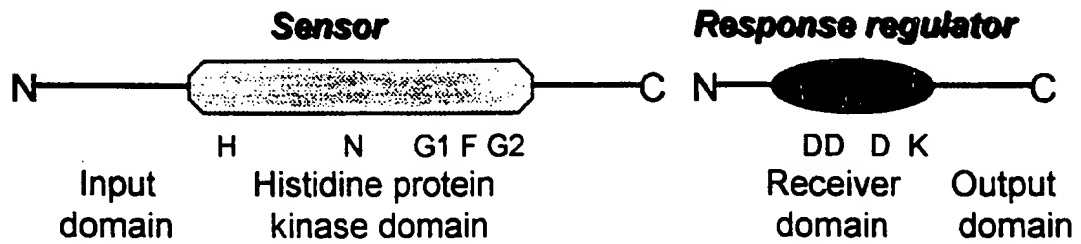


FIG. 3

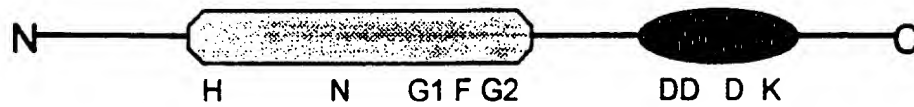
5/27

Comparison of bacterial two-component regulatory systems with DZ2

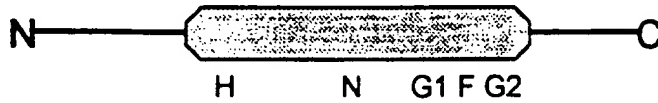
Bacterial two-component system



***Arabidopsis thaliana* ETR1 gene**



***Arabidopsis thaliana* ERS gene**



DZ2



FIG. 4

6/27

FIG. 5

TATATAAATACGGTTTAAACAGATATGTTCTGGTTATATAAATGTAATTCNATGTGCCNNTCAANTTTTATTTTNATNGT	78
TNTACTAGGGACATTAGTTTTTAAACNTTTTATATATCATGTGAACAAAAACNTTTTATATNTCAACTATGA	156
GCAATTATCTTATAGTGTCTTTTCCAGAAATTTGACGACAACCTAACTAAACAATTTAATTTTGACGTTAGTT	234
AAGTAAATTTATATAGATGATAAATTTGAGCAAGCACATTACGAACTGCGGATCAAGGAGAGTCACAATTTTAATCTTA	312
GGCTCTAGACGAACCTGCGGAGCAAGG -> DZ2BGENF	
XbaI	
CGTTATACACAAAAATTATCTAAATACTATATATATATACAGCTGCAATGCTACGATAATGATCAAAATGTTTATGTACTT	390
TTCAGCGAAAAATCTTTGTGCGCCATACATTACTGTGTTAATGAATCATTTAAATATGTGAAGGAGGAAAAAGAGTACAAAA	468
GGAGTTTGTGAGGCAITTCGCAGACACTGAAATGTGAATAATAATAAGGAATTGCCGAATTGATTTCTAGTTGGT	546
GAAGTGGTGAAAAATTGTATGTCCATTGCTTATAAACTATAAAATATAATATNTTNATATTATCACTNTGGACATTAG	624
TNNGATAGACCCCTAGCTAAAAATTTTAAAAAATTATACATTTCATTTTCTNAAGTACCAAACTTAATTTATCACAATCGGA	702
TAAAAATTGTTTAAGAAACCAATTACAAACTCAGCTTGTGGACTCTGAGAGAAACTAAGAGCTAGACATACGGTTAGTAG	780
TGTAGCCGCATTTTATATGCTTAATTTTGCTTAAGCATGACTTCTATGCTCCTTGATGATATTTTATTTAATATCCTAG	858
GACATAATGATTTGATAAAGATCTTATCAACCTTTCAACAAGACCAATTAGCTCAACAACAAAAATACTGAAAGTATAT	936

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8 / 27

FIG. 6

A) D22B cDNA sequence (top) -
D22 sequence (bottom)

TCGTCNAT

Dz2 sequence (bottom)

GGCAGCAGCAGAAATCGAAGATGGCAACAAAATCCATGGGAGATATCGAGAAAAATAAGAAGAAACTAAACGTGTTGATCGTC

TCGTCNAT

GATGATCCTGTAAACGGTAACTTCACGAGATTATCATCAATCGGTGA---ATTTCACAGACAGCTAAGAACGGTG
.....
GATGATGATCCACTAAACCTTTATAATTGATGAGAAGATCATCAAGCGATTGGGGGTATTTCACAGACAGCGAATAACGGTG

10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160

90 | 100 | 110 | 120 | 130 | 140 | 150 | 160
AGGAGGCAGTGAACATCCACCGCAGCGCAATGCATCTTTTGACCTTAATCCTAATGGATAAAGAAATGCCCGAGAGGGATGG
.....|.....|.....|.....|.....|.....|.....|.....
AGGAGGCAGTAAATCATCCACCGTGACCGCGGCTCATCTTTTGACCTTAATCCTAATGGATAAAGAAATGCCCGAGAGGGATGG

170 | 180 | 190 | 200 | 210 | 220 | 230 | 240

170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 | 250 |

ACTTTCGGCAACTAAGAGAAATGAAAGTGACGTCCTATGATTATTGGGGTGACGACACTGGCTGACCAATGAAGAG
| | | | | | | | | |

TGTTTCGCAACTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGGGGTGACTTCACTGGCTGACCAATGAAGAG
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |

9/27

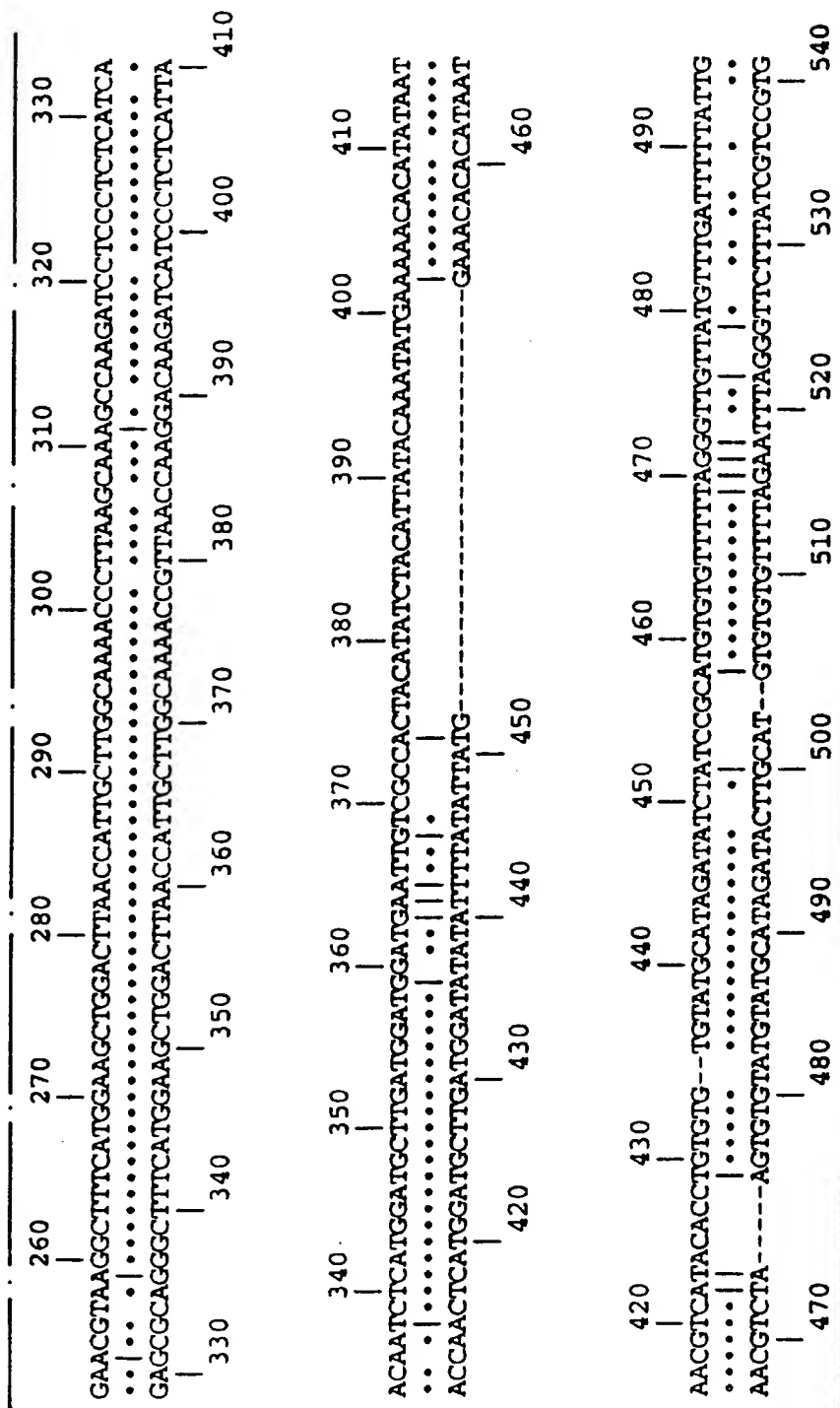
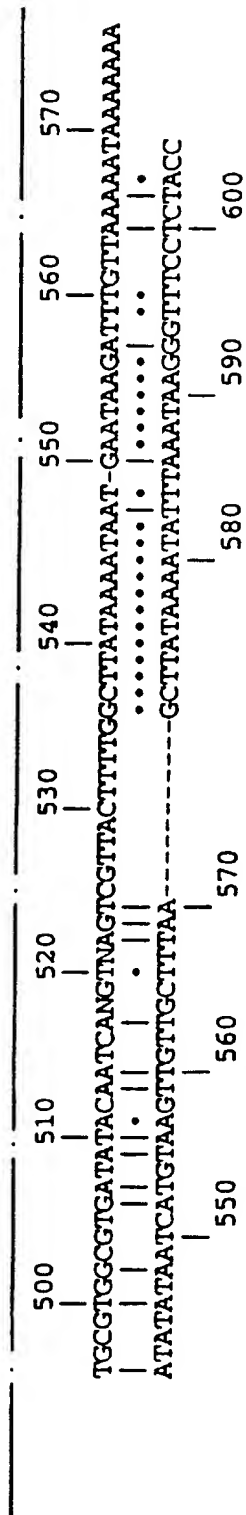


FIG. 6 CONT'D

10/27



**B) Dz2B peptide sequence (top) -
Dz2 peptide sequence (bottom)**

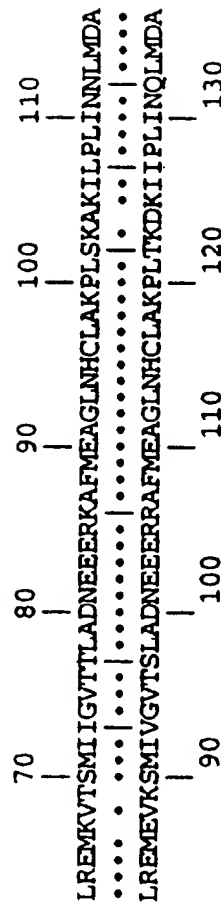
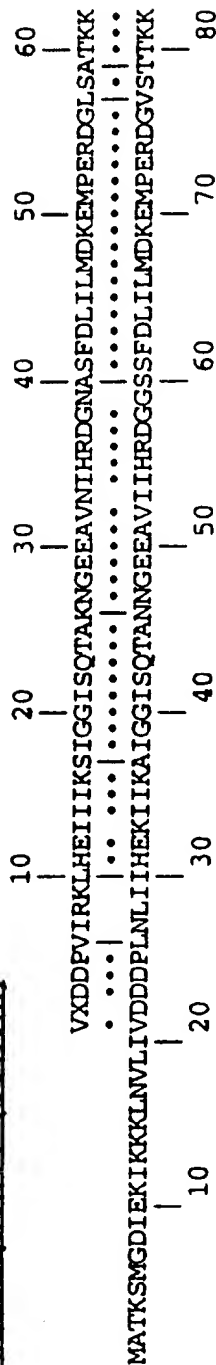
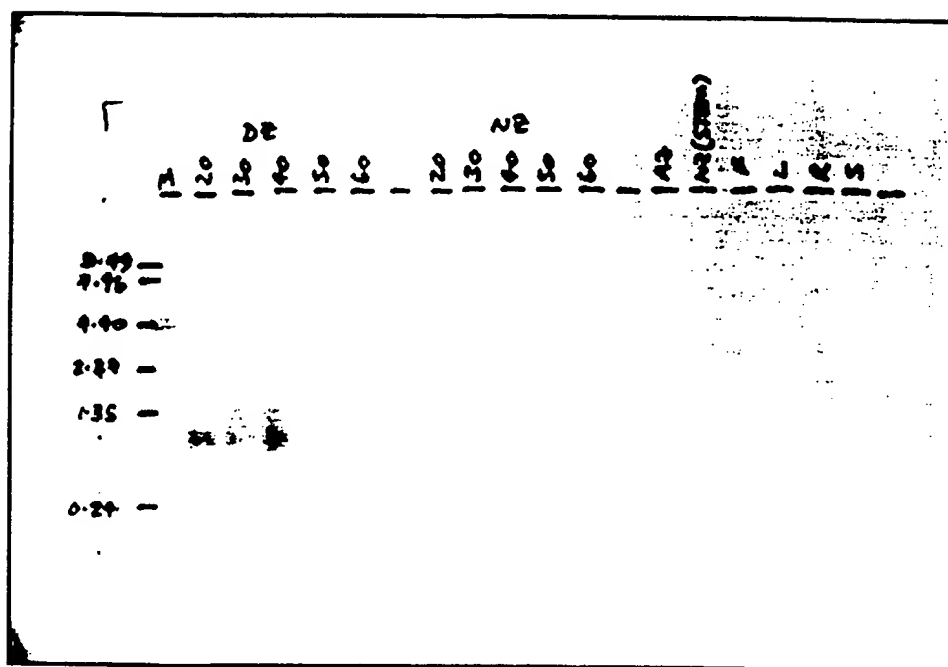


FIG. 6 CONT'D

11/27

FIG. 7

NORTHERN ANALYSIS OF EXPRESSION OF
DZ2B IN PODS AND OTHER TISSUES



DZ = POD DEHISCENCE ZONE (20 - 06 daa)

NZ = POD NON-ZONE

AZ = ABSCISSION ZONE

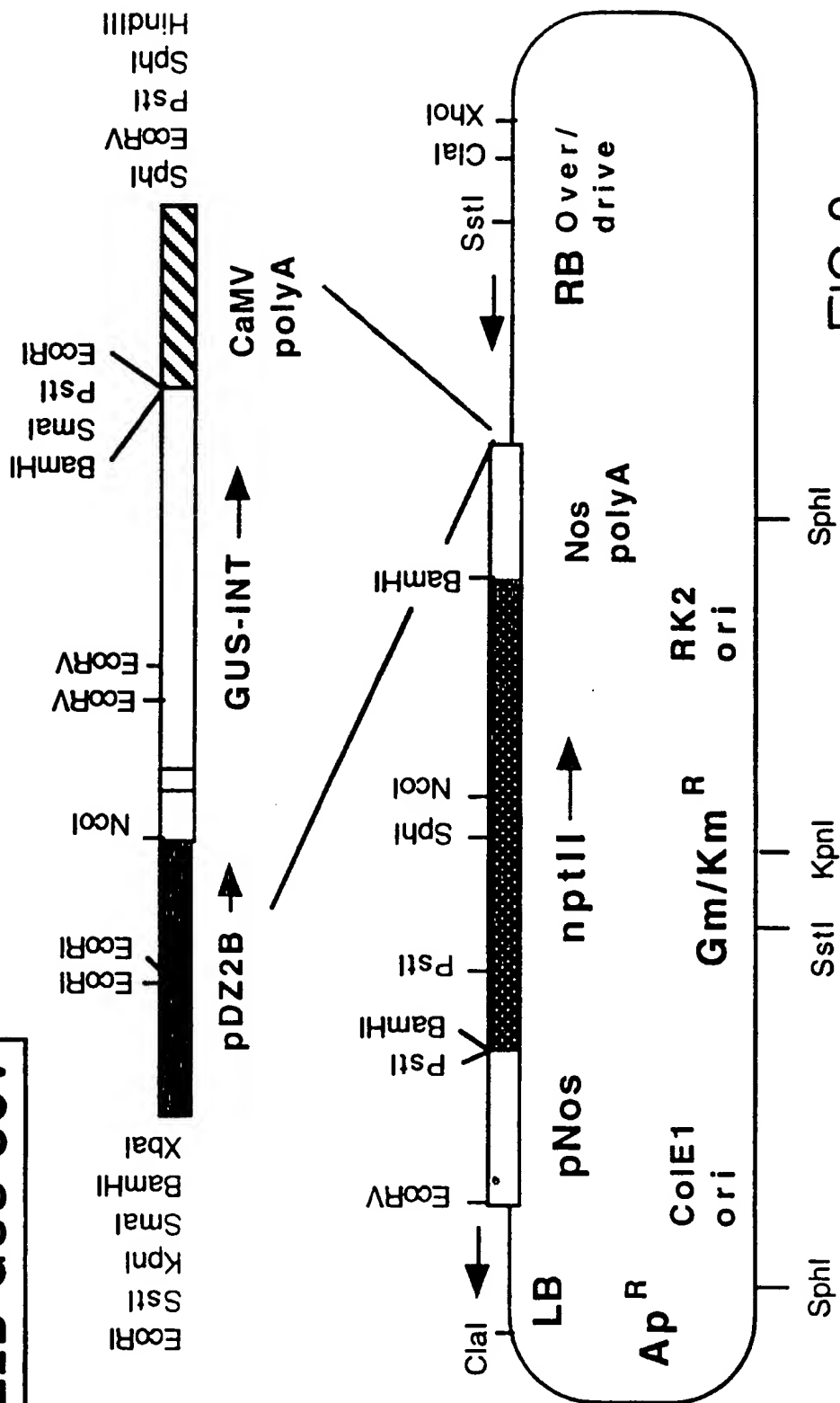
F = FLOWER

L = LEAF

R = ROOT

S = SEED

pDZ2B-GUS-SCV



F/G.8

FIG. 9

ATATATGTGATACAGATACATCTATATACAAAATTAAACACGAAACCATACATGACGGTGTGATCACACACGCACACA 78

CATAGAAACATAAACACGCAATAATTCTATACAGTTTAATTTCATTTTTTAACCTTACTTCTTTTTTTTGGTGAAGAT 156

TCTTGAGAGAAAGAAATCGAAGATGGCAACAAATCCACCGAGGTACCGAGAAACCAAGTCGATAGAAGTGAAGA 234
M A T K S T G G T E K T K S I E V K K

AGAAACTAATCAACGTGTTGATCGTCGATGATCCATTAAACCGTAGACTCCACGAGATGATCATCAAAAACGATCG 312
K L I N V L I V D D D P L N R R L H E M I I K T I G
<- CGATCG

<- CGAATAACGGTGAGGAGGCATTAATCA GW1
GAGGAATTTCTCAGACTGCAA AT3GW2
GAGGAATTTCTCAGACTGCAAAGAATGGCGAAGAGGCNGTGATCCTCCACCGTGACGGCGAAGCATCTTTTCGACCTTA 390
G I S Q T A K N G E E X V I L H R D G E A S F D L I

TTCTAATGGATAAGGAAATGCCCTGAGAGGGATGGAGTTTCGACAAATTAAGANGCTAAGAGAAATGAAAGGACGTCAA	468
L M D K E M P E R D G V S T I K X L R E M K G T S M	
TGATCGTTGGGTAACGTCAGTAGCTGACCAAGAAGAGCGTAAGGCTTTTATGGAAGCTGGGCTCAACCATTTGCT	546
I V G V T S V A D Q E E E R K A F M E A G L N H C L	
TGGAATAACCCCTTAACCAAGGCCAAGATCTTCCCGCTCATTAGCCACCTCTTCGATGCTTGATGATGAAGGCTCATT	624
E K P L T K A K I F P L I S H L F D A .	
AATGTATCTATATTTTCAATCATGAATCACCTACACGTGTATTGACACAAAAATCTGCATTGTGTGATATAGGG	702
TTTCTCATATCTATGTTGATTTATTTTCTTATCGTCCGAGGTAAATCATGCAAGTCATTCTTTTGGCTAATAAAA	780
TATTAAAAAAGGTTTCTCAAAAAAATAAAAAA	818

14/27

FIG. 9 CONT'D

15/27

A) DZ2A13 peptide sequence (top)
DZ2 peptide sequence (bottom)

FIG. 10

10	20	30	40	50	60	70	80
MATKSTGGTEKTSIEVKKKLINVLIVDDDPNRRRLHEMI							
IKTIGGISQTAKNGEEXVILHRDGEASF							
DLILMDKEMPERDG							
...
MATKSMGDIKIKKKLNVLI							
VDDDPNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDG							
10	20	30	40	50	60	70	80

90	100	110	120	130	140
VSTIKXLREMKGTSMIVG					
TSVADQEEERKAFMEAGLNHCL					
LEKPLTKAKIFPLISHLFDA					
...
VSTTKKLREMEVKSMIVG					
TSVADQEEERKAFMEAGLNHCL					
AKPLTKDKIIP					
LNQLMDA					
80	90	100	110	120	130

16/27

B) DZ2AT3 peptide sequence (top)
DZ2B peptide sequence (bottom)

10	20	30	40	50	60	70	80
MATKSTGGTEKTSIEVKKKLINVLIVDDDDPLNRRRLHEMI	IKTTIGGISQTAKNGEEXVILHRDGEASFDLILMDKEMPERDG						
• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •
VXDDPVIRKLHEIIKSIGGISQTAKNGEAEVNIHRDGNASFDLILMDKEMPERDG							
10	20	30	40	50			

90	100	110	120	130	140
VSTIKXLREMKGTSMIVGVTSVADQEEERKAFMEAGLNHCLEKPLTKAKIFPLISHLFDA					
• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •
LSATKKLREMKVTSMIIGVTTLADNEEERKAFMEAGLNHCLEKPLSKAKILPLINNLMDA					
60	70	80	90	100	110

FIG. 10 CONT'D

FIG. 11

GTAAATGCGACTACTATAGGACGCGTGGTCGACGGCCCGGCTGGTCCCTCATTCGTATTGGGCCCCAATGGGCTACT 78
 CACTAGTAGGGCACGCGTGGTCG -> ATDZ2F
 SpeI
 AAAACAGTTCACGATTGTTTTTTTTTTTTTTTAAATTTTAAACATGTATGTGGGATATTTGGCTATAAATTATG 156
 TAAAAAATTTCACGATAGATTGTTGAATTTTGAATTTTCGAGTTAAATAATCTTCAAAATTACCTCACATTACAAAAA 234
 GGTAAGACTGTTGAAAAAATAAGCTCTCTATAAAACACTAGACAATAACAAAAATACGTAATCGCTAAAGAACCTAAATT 312
 ATGATTTTATTATCTTTCTTCCTTTTCCGTGAGTATAAGCCATTTTTCATAGTAAAGCATTACGAATACGACATTG 390
 AACACTACTGACATATAAAGTAGTAGATTTTGATGGGTTAACTTGATGCTTAATTTGCTTAAGCATGAACCTCAATG 468
 CTTTATAAAGTACTTCATGAGAAATATTCCTCGTTCTATACTAGCAGAAGGGTTCGATAGTGATTTTACAACCCGTTT 546
 AACAAAAACCTTTAAACCCCAAAAAACCAAGAAATGAAAGTATCTAAACTTGATTATACATTTCTTGCTAAATTATCAA 624
 ATAACATACTCTCTTTTGTACTTATAAACGATATGAAAGAAAAATAAAGAACATAGAATCTTTATTATGATCT 702

AGAAAGAAATTAAAGAAATATATATATTTTTCATTTCTACTCATGTTTCTTATACATTTCTTAAATTGTT	780
CACCATTTTGATTTACTTGTCTTCATATAGTTTGTGTTATACAACTCACTTAGAATAATGTAGATTACATTTTCAGCCAA	858
ATTTCATGTAAGATGCTTTTCTTTGTGAAGTTTAAATGCTTTCTTTTTCACCTTTTCTTTCTTAACTATAAAT	936
CTTGATCGAATGCCCTTCTTTAGAACATAAAGATCTTCTTTTAAATCCAAATCGTAGGCCACTATTTCATTATACT	1013
TATGTAATATATGTGATACAGATACATNTATATACAAATTAACACGAAACCATAACATGCACGGTGTGATCACACACG	1092
CACACACATAGAAACATAAACACCGCAATAATTCTTATACAGTTTAAATTTTCACTTTTAACTTCTTTTCTTTTGTGT	1170
18/27	
NcoI	
<- CTTGAGAGAAAAGAAATCGACCATGGA	
GAAGATTCTTGAGAGAAAAGAAATCGAAGATCGCAACAAAATCCACCGGAGGTACCGAGAAAACCAAGTCGATAGAAG	1248
M A T K S T G G T E K T K S I E V	
TGAAGAAGAACTAATCAACGTGTTGATCGTGTGATGATCCATTAAACCGTAGACTCCACGAGTGTGCATCAAAA	1324
K K K L I N V L I V D D D P L N R R L H E C H Q ->	

FIG. 11 CONT'D

19/27

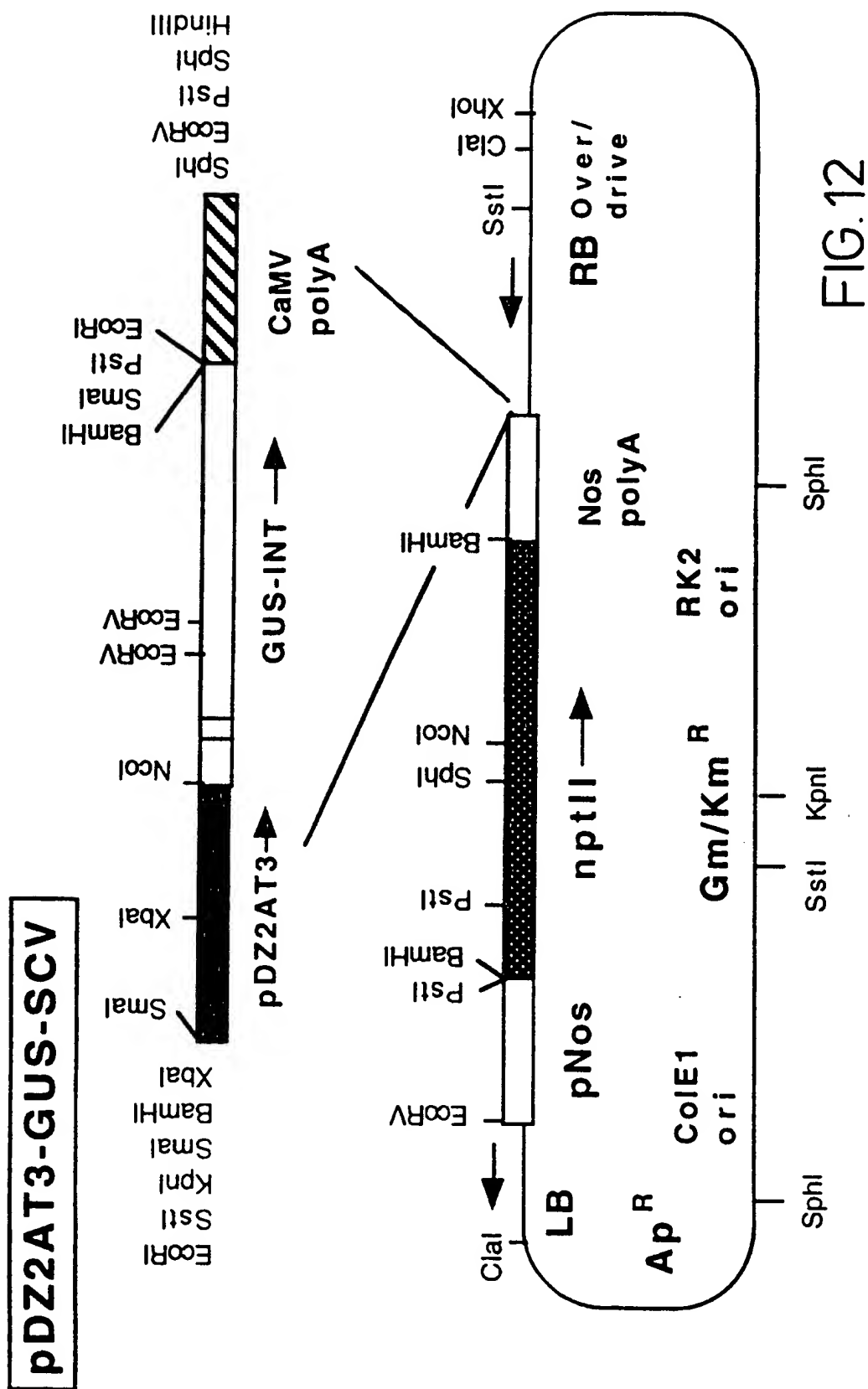


FIG.12

20/27

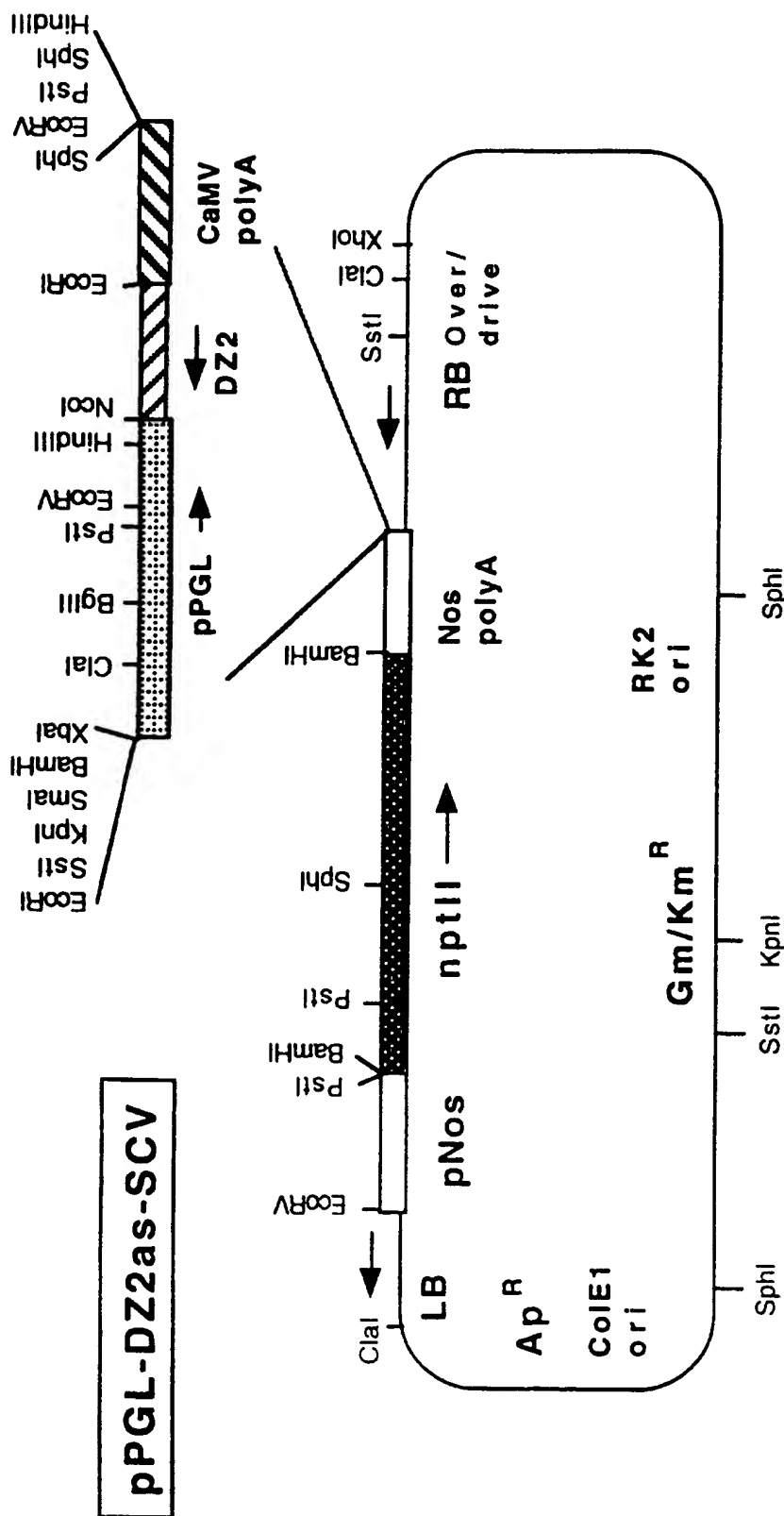


FIG. 13A

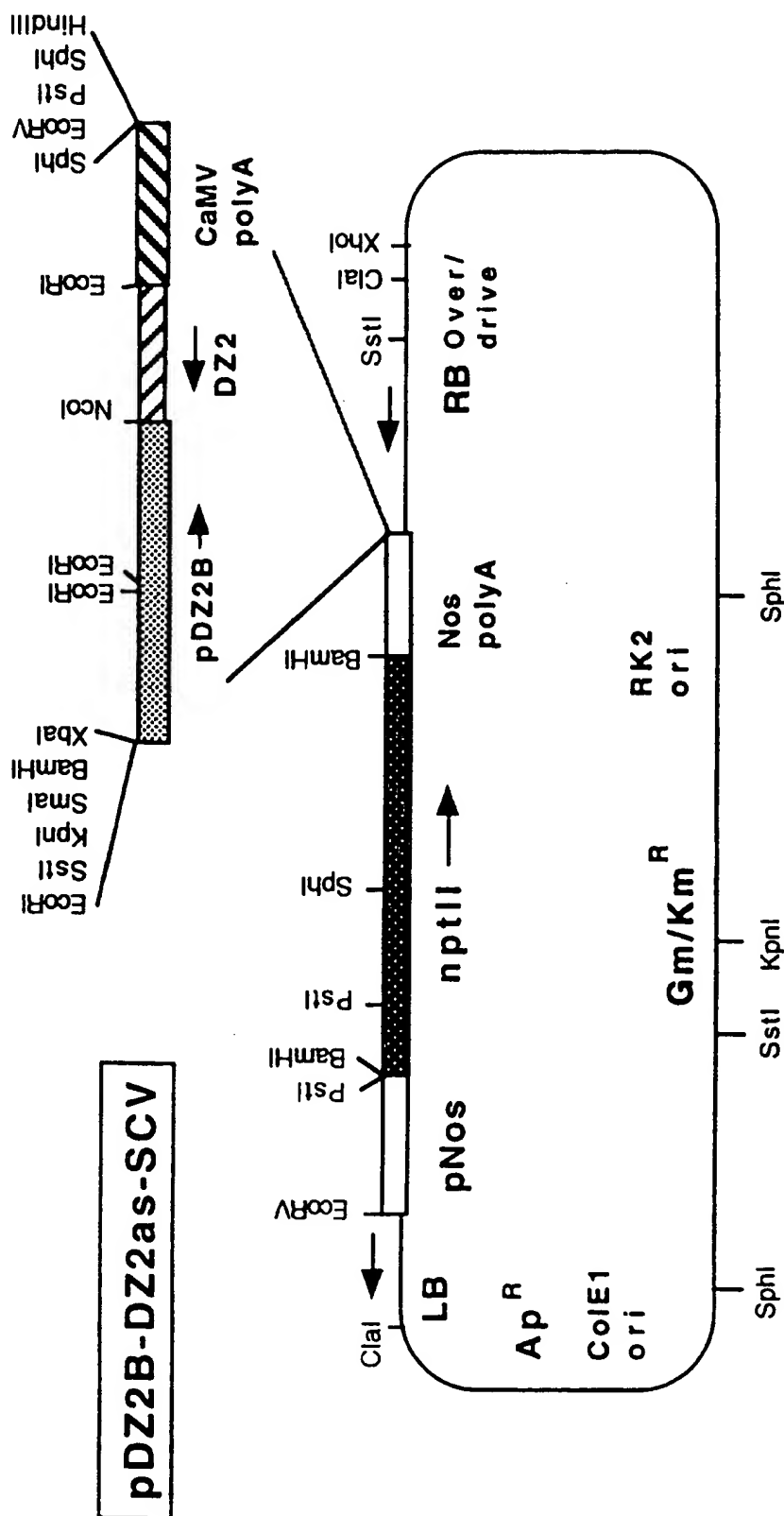


FIG. 13B



FIG. 15

GGCATCAGGAGGTACCCGTAATAATCCACCATACAACAAAGTTCTGTGAAAGTCTCCCA	60
AAACTGCCAAAGAGTCTCATATTAGTTCTTACTCTCAGAAATAAACACAGTGTTTCTGAA	120
AAGATTAGCGTTTCAAAACCCGAAATGGCCCGTTGTTCATGGAAGTCTTGCCTATTTTCTTA	180
M A R C H G S L A I F L	12
TGCGTTCTTTTGATGCTCGCTTGCTGCCAAGCTTTGAGTAGCAACGTAGATGATGGATAT	240
C V L L M L A C C O A L S S N V D D G Y	32
GGTCATGAAGATGGAAGCTTCGAAACCGATAGTTTAATCAAGCTCAACAACGACGACGAC	300
G H E D G S F E T D S L I K L N N D D	52
GTTCCTTACCCTTGAAAAGCTCCGATAGACCCCACTACCGAATCATCAACTGTTAGTGTTCG	360
V L T L K S S D R P T T E S S T V S V S	72
AACTTCGGAGCAAAAGGTGATGGAAAAACCGATGATACTCAGGCTTTCAGAAAGCATGG	420
N F G A K G D G K T D D T Q A F K K A W	92
AAGAAGGCATGTTCAACAAATGGAGTGACTACTTTCTTGATTCCCTAAAGGGAAGACTTAT	480
K K A C S T N G V T T F L I P K G K T Y	112
CTCCTTAAGTCTATTAGATTTCAGAGGCCCATGCAAAATCATACGTAGCTTCCAGATCCTA	540
L L K S I R F R G P C K S L R S F Q I L	132
GGCACTTTATCAGCTTCTACAAAACGATCGGATTACAGTAATGACAAGAACCACTGGCTT	600
G T L S A S T K R S D Y S N D K N H W L	152

24/27

ATTTGGAGGACGTTAATAATCTATCAATCGATGGCGGCTCGGCGGGATTGTTGATGGC 660
 I L E D V N N L S I D G G S A G I V D G 172

 ACGGAAAAATCTGGTGCAAACTCATGCAAAATCGACAAATCTAAGCCATGCACAAAA 720
 N G K I W W Q N S C K I D K S K P C T K 192

 GCGCCAACGGCTCTACTCTCTACAACCTAAACAATTGGAATGTGAAGAAATCTGAGAGTG 780
 A P T A L T L Y N L N N L N V K N L R V 212

 AGAAATGCACAGCAGATTTCGATTGAGAAATGCAACAGTGTGATGTTAAGAAT 840
 R N A Q Q I Q I S I E K C N S V D V K N 232

 GTTAAGATCACTGCTCCTGGCGGATAGTCCCAACACGGATGGTATTCATATCGTTGCTACT 900
 V K I T A P G D S P N T D G I H I V A T 252

 AAAACATTTCGAATCTCCAATTTCAGACATTGGGACAGGTGATGATTCATATCCATTGAG 960
 K N I R I S N S D I G T G D D C I S I E 272

 GATGGATCGCAAAATGTTCAAATCAATGATTTAACTTGGGCCCCGGTCATGGCATCAGC 1020
 D G S Q N V Q I N D L T C G P G H G I S 292

 ATTGGAAGCTTGGGGATGACAAATTCCAAAGCTTATGTATCGGGAATTAATGTGGATGGT 1080
 I G S L G D D N S K A Y V S G I N V D G 312

FIG. 15 CONT'D

25/27

GCTACGCTCTCTGAGACTGACAATGGAGTAAGAAATCAAGACTTACCAGGGAGGTCAGGA 1140
A T L S E T D N G V R I K T Y Q G G S G 332

ACTGCTAAGAACAATTAAATTCCAAACATTCGTATGGATAATGTCAAGAAATCCGATCATA 1200
T A K N I K F Q N I R M D N V K N P I I 352

ATCGACCAGAACTACTGCGGACAAGGACAAATGCGGAACAACAAGAAATCTGCGGTTCAAGTG 1260
I D Q N Y C D K D K C E Q Q E S A V Q V 372

AACAATGTCGTCATCGGAACATACAAGGTACGAGCGCAACGGATGTGGCGATAATGTTT 1320
N N V V Y R N I Q G T S A T D V A I M F 392

AATTGCAGTGTGAAATATCCATGCCAAGGTATTGTGCTTGAGAAATGTGAACATCAAAGGA 1380
N C S V K Y P C Q G I V L E N V N I K G 412

GGAAAAGCTTCTTGCAAAAATGTCAATGTAAAGGATAAAGGCACCGTTTCTCCTAAATGC 1440
G K A S C K N V N V K D K G T V S P K C 432

CCTTAATTACTAAGTTGATTATGTAATATACATAAAATACGTATTATATGTGGTTATAGAT 1500
P 433

GCCATCTATATCCTTATCTACGATTGATTCTCGATATATAGAAACTAAGGATTAT 1560

GGGAATATACATAACAATAGTTGAGATAATTGTTGCTCTTGATATATGGTTCACTGAAGTTGA 1620

TTGCTTGTCACGAATAAATGAATAATGTGCTTTGTC 1657

FIG. 15CONT'D

26/27

646679-001956

aggtgaccggttgctgatggcaatgtgctgggtcaagcgagaggttagacggtggcttgga
V T V A D G N V L V K R E V D G G L E T
cagttaaagtcaaattgccagctgtcattagcgccgacttgcggtcaatgagccgcggt
V K V K L P A V I S A D L R L N E P R Y
acgctactctgcccataatcatgaaggccaagaagaagcccatcaaaaagctcacagcca
A T L P N I M K A K K K P I K K L T A T
cagatgtcgggtgtggacttggcgccacgtcaacaagtgttgagcgtagaagacccgcca
D V G V D L A P R Q Q V L S V E D P P T
ccagacaggctggttccattgtgcctgatgtcgacactctcatcaccaagttgaaagaaa
R Q A G S I V P D V D T L I T K L K E K
agggtcattttgtaatgcaatgtcaccaatacagttgttttagttcttacaattcttcgt
G H L *
gaggttttcagctgttaccaataatattttttcaaaatcgattttattttacttgtaatt

taaaagatcaaataattaatacaatgaacatttttgtaacagcaatcttttttttatattt

tggagatttcatcgacttatgtcataattatttttatcaatttattgttggttgtagtg

atataataaagtatgttttctgggtcaaaa

FIG. 16

27/27

OSR79 306bp

```

5'      88ttgggtcgaaccataggtggaaagcttcttctctctcgcttgacaaatcctctggtt      .
      L G R T I G G K L L S L S L D K S S G S      .
      .      .      .      .      .      .      .      .      .      .
      cgggttttcagtcgccatcaggagtttctctatggtaaagctgaggttcaaatgaaacttg      .
      G F O S H Q E F L Y G K A E V O M K L V      .
      .      .      .      .      .      .      .      .      .      .
      tccctggtaactctgtggaacagtcacaacattcttctttaaatacccggaactacat      .
      P G N S A G T V T F Y L K S P G T T W      .
      .      .      .      .      .      .      .      .      .      .
      gggatgagatcgatttcgagttcttgggaaacataagtgggccatccctatactctccata      .
      D E I D F E F L G N I S G H P Y T L H T      .
      .      .      .      .      .      .      .      .      .      .
      ctaatgtttacacacgaaggctcttgagagacaaagaacagcagtttcatctatggttcgac      .
      N V Y T R R L W R Q R T A V S S M V R P      .
      .      .      .      .      .      .      .      .      .      .
      ccgacc      3'
      D

```

FIG. 17